



SEQUENCE LISTING

<110> ~~C. type 17~~ Research Foundation  
Chang, Yung-Fu

<120> Ehrlichia canis Genes for Vaccine Development

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<170> PatentIn version 3.1

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agt ata 96  
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Ser Ile  
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ttt tgt aaa gta aca ggt tat gga ggt aca gta aga aca agt  
aat ata 144  
Phe Cys Lys Val Thr Gly Tyr Gly Gly Thr Val Arg Thr Ser  
Asn Ile  
35 40 45

tca aat tct aaa ata ggt aac act att att aaa gtc aga ttt  
aat gca 192  
Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe  
Asn Ala  
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gat ata cac aaa caa ctg cca tgg aaa ttc tat cca gaa gta

tct cat 240  
 Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val  
 Ser His  
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gta ttt gta aaa cca gga gaa caa aaa ttg att ttc tac cgc  
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 Ala Glu

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acc aaa caa aca tta tac cct cat caa aaa act ata atg cca  
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 Val Ser

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140

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 Asn Ile  
 35 40 45

Ser Asn Ser Lys Ile Gly Asn Thr Ile Ile Lys Val Arg Phe  
 Asn Ala  
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Asp Ile His Lys Gln Leu Pro Trp Lys Phe Tyr Pro Glu Val  
 Ser His  
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Val Phe Val Lys Pro Gly Glu Gln Lys Leu Ile Phe Tyr Arg  
 Ala Glu  
 85 90  
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Asn Leu Leu Asp Glu Asp Thr Ser Gly Met Ala Val Tyr Asn  
 Val Thr  
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Pro His Lys Val Gly Lys Tyr Phe Asn Lys Val Ala Cys Phe  
Cys Phe

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Thr Lys Gln Thr Leu Tyr Pro His Gln Lys Thr Ile Met Pro  
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25

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Ala Val  
35 40 45

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gta gga 192  
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Val Gly  
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Gly Thr  
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Gly Asn  
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95

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Phe Asn Ala Ser Thr Ser Gln Phe Cys Thr Ile Tyr Tyr Glu  
Leu Ile  
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Pro Lys Gln Tyr Leu Ser Leu Ala Met Asp Ile Glu Ser Asp  
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Lys Val  
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140

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Asn Ile  
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Glu Val  
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Gln Tyr Tyr Gly Lys Ile Pro Ser Asn Asn Lys Lys Pro Ser  
Ser Gln  
225 230 235  
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gtt agg gta gaa cca ccg cat aaa aca aat atg act tta aca  
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250

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270

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Val Ile  
290 295 300

aac aat cca ata gtt aca tcg ata aaa aca gat tat aat tac  
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Leu Thr  
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gac agc gat aat tac ctt tcc att gaa gct ata cct aaa aac  
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Gly Ile  
325 330

335

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Asn Tyr  
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 Tyr Lys  
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 Ile Ser  
 370 375 380

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 Glu Ile  
 385 390 395  
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 Ala Val  
 35 40 45

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 50 55 60

Tyr Ser Gly Leu Ala His Phe Phe Glu His Leu Met Phe Ser  
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Glu Lys Phe Pro Asn Leu Ile Ser Thr Leu Ser Asn Ile Gly  
 Gly Asn  
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 Val Asn  
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aat aca tat gca aat gat ctc aat att aac ata aaa gaa gct  
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 Thr Thr  
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 Pro Thr

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 Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu  
 Asn Glu  
 65 70 75  
 80

gga tca aaa aac aac tat gct ctc agt ttt gca caa caa tta  
 gaa ggc 288  
 Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu  
 Glu Gly  
 85 90  
 95

aaa ggt ata gac tta aaa ttt gat ata gac cta gac aat ttt  
 tat ata 336  
 Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe  
 Tyr Ile  
 100 105 110

tca tta aaa acc tta tca gaa aac ttt gaa gaa gcc cta gtt  
 tta ctc 384  
 Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val  
 Leu Leu  
 115 120 125

agt gat tgc ata ttc aac acc gtc aca gat caa gaa ata ttc  
 aat aga 432  
 Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe  
 Asn Arg

130	135	140
ata ata gca gaa cag att gca cat gtt aaa tca tta tat tct		
gct cct 480		
Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser		
Ala Pro		
145	150	155
160		
gaa ttt ata gct aca aca gaa atg aat cac gct ata ttc aaa		
ggg cac 528		
Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys		
Gly His		
	165	170
175		
cca tat tct aac aaa gtt tac ggg aca tta aat aca atc aat		
aat atc 576		
Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn		
Asn Ile		
	180	185 190
aac cag gaa gac gtt gca tta tat ata aaa aat agt ttt gac		
aag gaa 624		
Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp		
Lys Glu		
195	200	205
caa atc gtt atc agc gca gca gga gat gta gat cca aca cag		
cta tca 672		
Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln		
Leu Ser		
210	215	220
aat tta cta gat aaa tat att ctt tcc aaa ttg cca tct ggt		
aat aac 720		
Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly		
Asn Asn		
225	230	235
240		
aaa aat acc ata cca gat acg act gtt aat aga gaa gac aca		
tta tta 768		
Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr		

Leu Leu

245

250

255

tat gta cag aga gat gta cca caa agt gtc ata atg ttt gct  
aca gac 816  
Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala  
Thr Asp  
260 265 270

aca gta cca tat cac agc aaa gac tat cat gca tca aac ttg  
ttc aat 864  
Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu  
Phe Asn  
275 280 285

act atg cta ggc gga tta agt ctc aat tca ata tta atg ata  
gaa tta 912  
Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile  
Glu Leu  
290 295 300

aga gac aag tta gga tta aca tac cat agt agc agt tca cta  
tct aac 960  
Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu  
Ser Asn  
305 310 315  
320

atg aat cat agt aat gtg cta ttt ggt aca ata ttc act gat  
aat acc 1008  
Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp  
Asn Thr  
325 330  
335

aca gta aca aaa tgt ata tcc gtc tta aca gat att ata gag  
cac att 1056  
Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu  
His Ile  
340 345 350

aaa aag tat gga gtt gat gaa gac act ttt gca att gca aaa  
tct agt 1104

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys  
 Ser Ser  
 355 360 365

att acc aac tct ttt att tta tct atg tta aat aac aat aat  
 gtt agt 1152  
 Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn  
 Val Ser  
 370 375 380

gag ata ttg tta agc tta caa tta cac gat cta gat ccg agt  
 tat att 1200  
 Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser  
 Tyr Ile  
 385 390 395  
 400

aat aaa tac aat tct tac tac aaa gca ata aca ata gaa gaa  
 gta aat 1248  
 Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu  
 Val Asn  
 405 410  
 415

aaa att gcc aag aaa att tta tct aat gaa tta gta ata att  
 gaa gta 1296  
 Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile  
 Glu Val  
 420 425 430

gga aaa aac aat aac ata aat ggc aaa caa ata gat gct aaa  
 aaa cac 1344  
 Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys  
 Lys His  
 435 440 445

ata ctt ggt  
 1353  
 Ile Leu Gly  
 450

<210> 7  
 <211> 451  
 <212> PRT  
 <213> Ehrlichia canis

<400> 7

Met Arg Asn Ile Leu Cys Tyr Thr Leu Ile Leu Ile Phe Phe  
 Ser Phe  
 1 5 10  
 15

Asn Thr Tyr Ala Asn Asp Leu Asn Ile Asn Ile Lys Glu Ala  
 Thr Thr  
 20 25 30

Lys Asn Lys Ile His Tyr Leu Tyr Val Glu His His Asn Leu  
 Pro Thr  
 35 40 45

Ile Ser Leu Lys Phe Ala Phe Lys Lys Ala Gly Tyr Ala Tyr  
 Asp Ala  
 50 55 60

Phe Asp Lys Gln Gly Leu Ala Tyr Phe Thr Ser Lys Ile Leu  
 Asn Glu  
 65 70 75  
 80

Gly Ser Lys Asn Asn Tyr Ala Leu Ser Phe Ala Gln Gln Leu  
 Glu Gly  
 85 90  
 95

Lys Gly Ile Asp Leu Lys Phe Asp Ile Asp Leu Asp Asn Phe  
 Tyr Ile  
 100 105 110

Ser Leu Lys Thr Leu Ser Glu Asn Phe Glu Glu Ala Leu Val  
 Leu Leu  
 115 120 125

Ser Asp Cys Ile Phe Asn Thr Val Thr Asp Gln Glu Ile Phe  
 Asn Arg  
 130 135 140

Ile Ile Ala Glu Gln Ile Ala His Val Lys Ser Leu Tyr Ser  
 Ala Pro  
 145 150 155  
 160

Glu Phe Ile Ala Thr Thr Glu Met Asn His Ala Ile Phe Lys  
 Gly His  
 165 170  
 175

Pro Tyr Ser Asn Lys Val Tyr Gly Thr Leu Asn Thr Ile Asn  
 Asn Ile  
 180 185 190

Asn Gln Glu Asp Val Ala Leu Tyr Ile Lys Asn Ser Phe Asp  
 Lys Glu  
 195 200 205

Gln Ile Val Ile Ser Ala Ala Gly Asp Val Asp Pro Thr Gln  
 Leu Ser  
 210 215 220

Asn Leu Leu Asp Lys Tyr Ile Leu Ser Lys Leu Pro Ser Gly  
 Asn Asn  
 225 230 235  
 240



Lys Asn Thr Ile Pro Asp Thr Thr Val Asn Arg Glu Asp Thr  
Leu Leu

245

250

255

Tyr Val Gln Arg Asp Val Pro Gln Ser Val Ile Met Phe Ala  
Thr Asp

260

265

270

Thr Val Pro Tyr His Ser Lys Asp Tyr His Ala Ser Asn Leu  
Phe Asn

275

280

285

Thr Met Leu Gly Gly Leu Ser Leu Asn Ser Ile Leu Met Ile  
Glu Leu

290

295

300

Arg Asp Lys Leu Gly Leu Thr Tyr His Ser Ser Ser Ser Leu  
Ser Asn

305

310

315

320

Met Asn His Ser Asn Val Leu Phe Gly Thr Ile Phe Thr Asp  
Asn Thr

325

330

335

Thr Val Thr Lys Cys Ile Ser Val Leu Thr Asp Ile Ile Glu  
His Ile

340

345

350

Lys Lys Tyr Gly Val Asp Glu Asp Thr Phe Ala Ile Ala Lys  
Ser Ser

355

360

365

Ile Thr Asn Ser Phe Ile Leu Ser Met Leu Asn Asn Asn Asn  
 Val Ser  
 370 375 380

Glu Ile Leu Leu Ser Leu Gln Leu His Asp Leu Asp Pro Ser  
 Tyr Ile  
 385 390 395  
 400

Asn Lys Tyr Asn Ser Tyr Tyr Lys Ala Ile Thr Ile Glu Glu  
 Val Asn  
 405 410  
 415

Lys Ile Ala Lys Lys Ile Leu Ser Asn Glu Leu Val Ile Ile  
 Glu Val  
 420 425 430

Gly Lys Asn Asn Asn Ile Asn Gly Lys Gln Ile Asp Ala Lys  
 Lys His  
 435 440 445

Ile Leu Gly  
 450

<210> 8  
 <211> 663  
 <212> DNA  
 <213> Ehrlichia canis

<220>  
 <221> CDS  
 <222> (1)..(663)  
 <223> Protein translated from nucleotides 4,132 through  
 4,794 (mmpA).

<400> 8

atg aaa gct cat agc aca agt ata cgg aac ttt cag cct tta  
 gaa aga 48  
 Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu  
 Glu Arg

1 5 10  
 15

gct gct ata atc att gca gtg tta ggt tta gct gca ttc ttg  
 ttt gct 96  
 Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu  
 Phe Ala

20 25 30

gct gct gcc tgc agt gat cgt ttc caa aga ttg caa tta aca  
 aat cca 144  
 Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr  
 Asn Pro

35 40 45

ttt gta ata gca gga atg gtt ggc ctt gca gtt ctt tta gtt  
 gct tcc 192  
 Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val  
 Ala Ser

50 55 60

tta aca gca gca tta agt ata tgc tta act aaa agt aag caa  
 gtc aca 240  
 Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln  
 Val Thr

65 70 75

80

caa cat gct att aga cat cgc ttt gga tac gag tca agc act  
 tct tct 288  
 Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr  
 Ser Ser

85 90

95

tct gta ctg ctt gca ata tca ata att tct tta tta ctt gct  
 gca gca 336  
 Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala  
 Ala Ala

100 105 110

ttt tgt gga aag ata atg ggt aat gac aac cca gat cta ttc  
 ttt agc 384  
 Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe  
 Phe Ser

115

120

125

aag atg caa gaa ctc tcc aat cca ctt gtt gtt gca gct att  
 gta gcc 432  
 Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile  
 Val Ala

130

135

140

gtt tct gtt ttc cta ctc tca ttc gta atg tat gct gca aag  
 aac att 480  
 Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys  
 Asn Ile

145

150

155

160

ata agt cca gat aaa caa act cac gtt att ata tta tct aat  
 caa caa 528  
 Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn  
 Gln Gln

165

170

175

act ata gaa gaa gca aaa gta gat caa gga atg aat att ttg  
 tca gca 576  
 Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu  
 Ser Ala

180

185

190

gta ctc cca gca gct ggc att gac atc atg act ata gct tct  
 tgt gac 624  
 Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser  
 Cys Asp

195

200

205

att tta gca gtg agc agc cgg gga tcc tct cag cat caa  
 663  
 Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln

210

215

220

<210> 9  
 <211> 221  
 <212> PRT  
 <213> Ehrlichia canis

<400> 9

Met Lys Ala His Ser Thr Ser Ile Arg Asn Phe Gln Pro Leu  
 Glu Arg  
 1 5 10  
 15

Ala Ala Ile Ile Ile Ala Val Leu Gly Leu Ala Ala Phe Leu  
 Phe Ala  
 - - -20 - - - 25 - - - 30

Ala Ala Ala Cys Ser Asp Arg Phe Gln Arg Leu Gln Leu Thr  
 Asn Pro  
 35 40 45

Phe Val Ile Ala Gly Met Val Gly Leu Ala Val Leu Leu Val  
 Ala Ser  
 50 55 60

Leu Thr Ala Ala Leu Ser Ile Cys Leu Thr Lys Ser Lys Gln  
 Val Thr  
 65 70 75  
 80

Gln His Ala Ile Arg His Arg Phe Gly Tyr Glu Ser Ser Thr  
 Ser Ser  
 85 90  
 95

Ser Val Leu Leu Ala Ile Ser Ile Ile Ser Leu Leu Leu Ala  
 Ala Ala

100

105

110

Phe Cys Gly Lys Ile Met Gly Asn Asp Asn Pro Asp Leu Phe  
Phe Ser

115

120

125

Lys Met Gln Glu Leu Ser Asn Pro Leu Val Val Ala Ala Ile  
Val Ala

130

135

140

Val Ser Val Phe Leu Leu Ser Phe Val Met Tyr Ala Ala Lys  
Asn Ile

145

150

155

160

Ile Ser Pro Asp Lys Gln Thr His Val Ile Ile Leu Ser Asn  
Gln Gln

165

170

175

Thr Ile Glu Glu Ala Lys Val Asp Gln Gly Met Asn Ile Leu  
Ser Ala

180

185

190

Val Leu Pro Ala Ala Gly Ile Asp Ile Met Thr Ile Ala Ser  
Cys Asp

195

200

205

Ile Leu Ala Val Ser Ser Arg Gly Ser Ser Gln His Gln  
210 215 220

&lt;210&gt; 10

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Ehrlichia canis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(417)

<223> Protein translated from complementary sequence  
 derived from nucle  
 otides 4,883 through 5,299 (partial lipoprotein  
 signal peptidase  
 homolog).

&lt;400&gt; 10

gat cag gta agt aaa tgg tat gta gta aat ttg ata gga gat  
 aaa ggt 48  
 Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp  
 Lys Gly  
 1 5 10  
 15

gta ata gag ata tta agc ttc ttg cgc ttt act aca gtg tgg  
 aat cct 96  
 Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp  
 Asn Pro  
 20 25 30

gga att agt ttt ggt ata tta aat aac ttt gaa tat agt aat  
 gtt gtt 144  
 Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn  
 Val Val  
 35 40 45

ttt tgt agt atc tcg att ttg att act tgt gtt tta tgc tac  
 tta ttt 192  
 Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr  
 Leu Phe  
 50 55 60

ata gta cag cca cat tat aga tta cct ctt gta atc att att  
 ggg ggg 240  
 Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile  
 Gly Gly  
 65 70 75  
 80

tca ata gga aat atc ata gat aga ata aga tat ggt gct gtc

tat gat 288  
Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val  
Tyr Asp

85

90

95

ttt ata gat ttt tat atc aat aac tta cat tgg cct gta ttc  
aac ctg 336  
Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe  
Asn Leu

100

105

110

gcg gat tct ttt ata ttt tta ggt ata gta ata ata atg gca  
aag agt 384  
Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala  
Lys Ser

115

120

125

aat aac cac atg aaa caa att aac tgt aac tcc  
417

Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser

130

135

<210> 11  
<211> 139  
<212> PRT  
<213> Ehrlichia canis

<400> 11

Asp Gln Val Ser Lys Trp Tyr Val Val Asn Leu Ile Gly Asp  
Lys Gly

1

5

10

15

Val Ile Glu Ile Leu Ser Phe Leu Arg Phe Thr Thr Val Trp  
Asn Pro

20

25

30

Gly Ile Ser Phe Gly Ile Leu Asn Asn Phe Glu Tyr Ser Asn



Val Val

35

40

45

Phe Cys Ser Ile Ser Ile Leu Ile Thr Cys Val Leu Cys Tyr  
Leu Phe  
50 55 60

Ile Val Gln Pro His Tyr Arg Leu Pro Leu Val Ile Ile Ile  
Gly Gly  
65 70 75  
80

Ser Ile Gly Asn Ile Ile Asp Arg Ile Arg Tyr Gly Ala Val  
Tyr Asp  
85 90  
95

Phe Ile Asp Phe Tyr Ile Asn Asn Leu His Trp Pro Val Phe  
Asn Leu  
100 105 110

Ala Asp Ser Phe Ile Phe Leu Gly Ile Val Ile Ile Met Ala  
Lys Ser  
115 120 125

Asn Asn His Met Lys Gln Ile Asn Cys Asn Ser  
130 135

<210> 12

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artifical Sequence: oligonucleotide

<400> 12

aggcttggtc aggggtgaaga agaatccaac gacaaaagct t

41

<210> 13

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide

<400> 13

aagcttttgt cgttggattc ttcttcaccc tgaacttgcc a

41